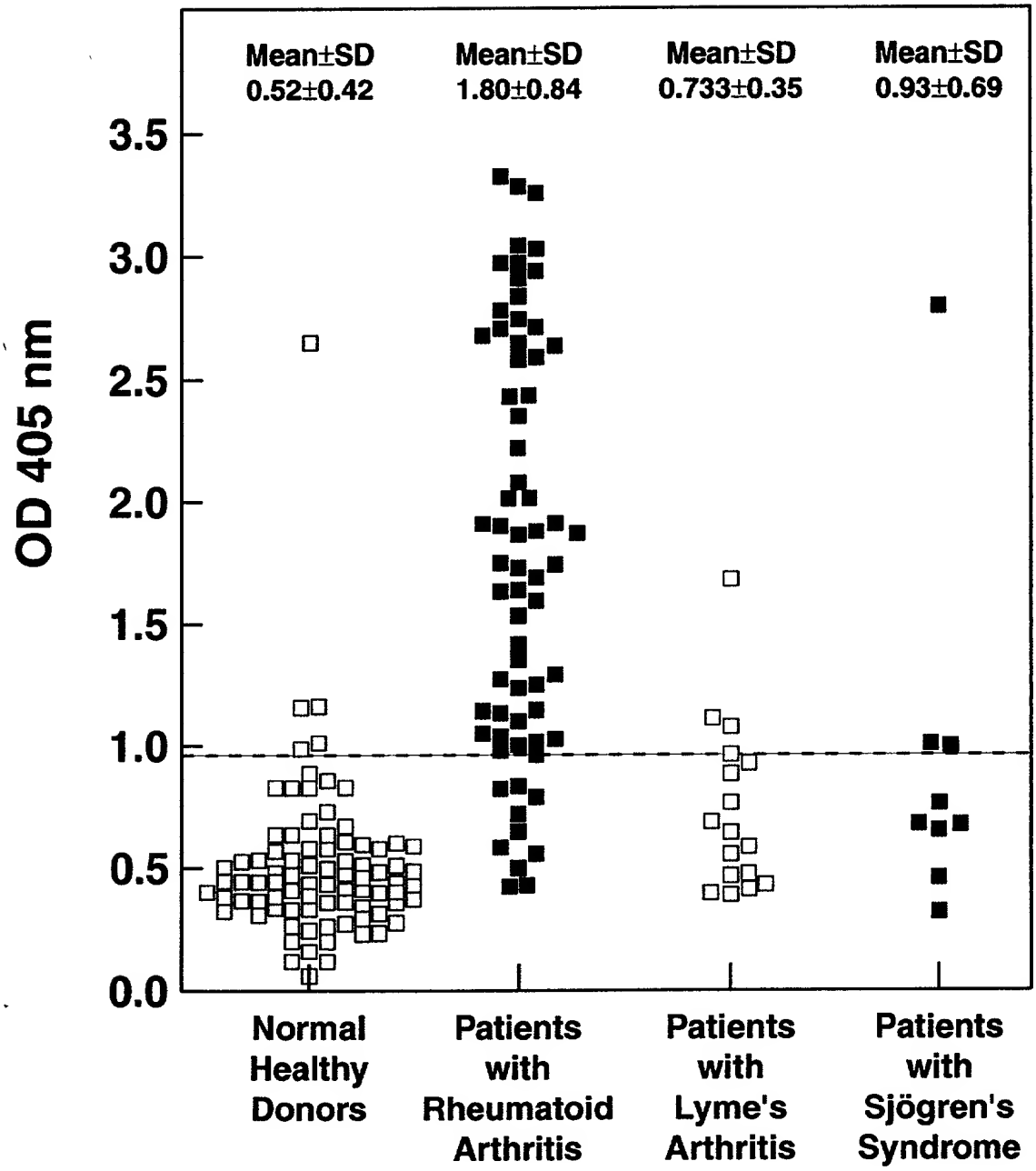

Mean±SD
0.52±0.42
Mean±SD
1.80±0.84
Mean±SD
0.733±0.35
Mean±SD
0.93±0.69
OD 405 nm
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Normal Healthy Donors
Patients with Rheumatoid Arthritis
Patients with Lyme's Arthritis
Patients with Sjögren's Syndrome

Fig. 1A

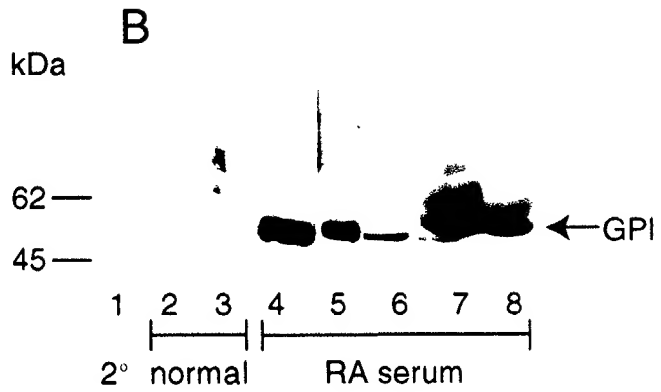


Fig. 1B

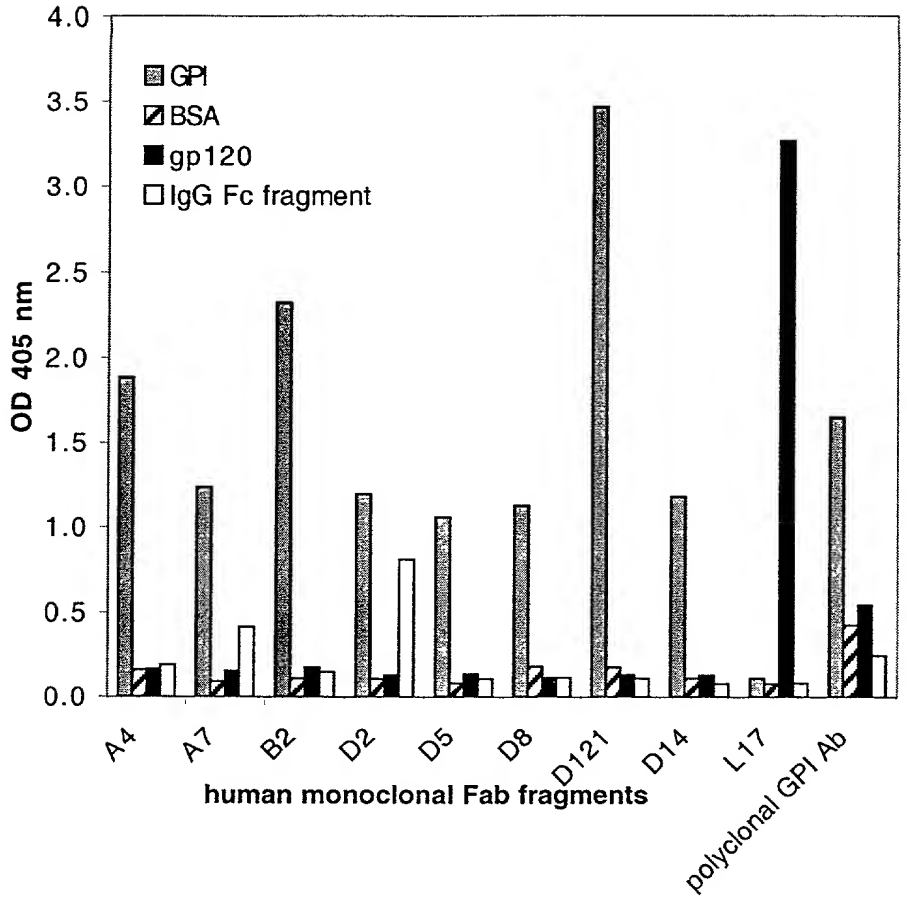

4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
OD 405 nm
GPI
BSA
gp120
IgG Fc fragment
A4
A7
B2
D2
D5
D8
D121
D14
L17
polyclonal GPI Ab
human monoclonal Fab fragments

Fig. 2

FIG. 3AL

Light Chain Variable AA Sequences

Name	SEQ ID NO:	FR1	CDR1	FR2
A4	1	PDSLAVSLGERATINC	KSSQSVFYTSNNKNYLA	WYQQKPGQPPKLLIY
D2	2	PSFLSASVGDRVTITC	RASQGISSYLA	WYQLKPGKAPKLLIY
D121	3	PGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY
B2	4	PDSLAVSLGERATINC	KSSQSVFYTSNNKNYLA	WYQQKPGQPPKLLIY
D14	5	PGTLSLSPGEGATLSC	RASQSVSSSYLA	WYQQRPGQAPRLLIY
D5	6	PGTLSLSPGEGATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY
A7	7	PGTLSLSPGERVTLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY

Name cont'd	CDR2	FR3	CDR3	FR4
A4	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	QQYYDSYT	FGQGTKLEIKRTVA
D2	AASTLQS	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	QQLNSYPLT	FGGGAKVGIRRTVA
D121	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPRT	FGQGTKVEIKRTVA
B2	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	QQYYDSYT	FGQGTKLEIKRTVA
D14	GASSRAT	GIPDRFSGSGSGTDFSFTISSLQPEDTGTYYC	QQYDNVPDT	FGQGTRLEIKRTVA
D5	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGTSPL	FGQGTRLEIKRTVA
A7	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPRT	FGQGTKVEIKRTVA

FIG. 3AH

Heavy Chain Variable AA Sequences

Name	SEQ ID NO.	FR1	CDR1	FR2	CDR2
A4	8	GGGVVQPGRSLKLSCAASGFTFS	SHGSH	WVRQAPGKGLEWVA	LLSSDGSNKFYIESVKG
D2	9	......AW..LR...V.....	..TM.	.....	..TM.
D121	10	..........R.....	.YTF.	.....	VI.Y..NK.Y.AD....
B2	11	GAEVRKPGTSVRISCRASGNTFT	GHHIH	WVRQAPGQGLQWMG	RINPTGGGVSLAQSFQD
D14	12	GGGLVQPGGSLRLSCATSGFIFN	SYAMN	WVRQAPGKGLEWVS	RISGNSGSTFYADSVKG
D5	13	GPGLVRPSQTLSLTCPVSPGSIK	GDSYFWS	WVRQPVGKGLEWIG	RIYGRGTTNYNRVFGS
A7	14	GAEVKKPGSSVKVSCRASGGTFS	RYAIS	WVRQAPGQGLEWMG	GIIPPFGPVNYAQKFQG

Name cont'd	FR3	CDR3	FR4	VH gene
A4	RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI	SLVGTTAFNY	WGQGTLVTVSS	VH3
D2	.....R.....LS...PE.....TN	.E..A...D.	.....	VH3
D121	.....VE.....	.I.....		VH3
B2	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR	PRFNMIREPLDL	WGQGTVVTVSS	VH1
D14	RFTISRDNSKNTAFLRMNSQRAEDTAVYYCAK	DLSSGAYYYYGMDV	WGQGTTVTVSS	VH3
D5	RVSMSVDMSRSQFFLELRDVTAADTAVYYCAR	DKGSEYSYFDP	WGQGIVVNVFS	VH4
A7	RVTITADDSTNTAYMGLSSLRSGDTAVYYCAR	VAYDGSGYYNNIPKIYYYSYMDV	WGKGTTVTVSS	VH1

FIG. 3B

Name	SEQ ID NO:	FR1	CDR1	FR2	CDR2
A4	8	GGGVVQPGRSLKLSCAASGFTFS	SHGSH	WVRQAPGKGLEWVA	LLSSDGSNKFYIESVKG
D2	9	......AW..LR...V.....	..TM.		..TM.
D121	10	..........R.....	.YTF.		VI.Y..NK.Y.AD....
DP-46		..........R.....	.YAM.		VI.Y.....AD....
B2	11	GAEVRKPGTSVRISCRASGNTFT	GHHIH	WVRQAPGQGLQWMG	RINPTGGGVSLAQSFQD
DP-7		....K...A..KV..K...Y...	SYYMH	.....E...	I...S..ST.Y..K..G
D14	12	GGGLVQPGGSLRLSCATSGFIFN	SYAMN	WVRQAPGKGLEWVS	RISGNSGSTFYADSVKG
VH26		.....A...T.S	....S		A...SG...Y.....
D5	13	GPGLVRPSQTLSLTCPVSPGSIK	GDSYFWS	WVRQPVGKGLEWIG	RIYGRGTTNYNRVFGS
IGHCAK		.....K.....T..G...S	SG..Y..	.I...A.....	...TS.S....PSLK.
A7	14	GAEVKKPGSSVKVSCRASGGTFS	RYAIS	WVRQAPGQGLEWMG	GIIPPFGPVNYAQKFQG
VH1-69		.....K.....	S....	.....	....I..TA.....

FIG. 3B CONT'D

Name cont'd	FR3	CDR3	FR4	VH gene
A4	RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI	SLVGTTAFNY	WGQGTLVTVSS	VH3
D2	.....R.....LS...PE.....TN	.E..A...D.	.....	VH3
D121	.....VE.....	.I.....		VH3
DP-46	.....R.....AE.....R			
B2	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR	PRFNMIREPLDL	WGQGTVVTVSS	VH1
DP-7	..TM...T.TS..YM...S.RS....V.Y...			
D14	RFTISRDNSKNTAFLRMNSQRAEDTAVYYCAK	DLSSGAYYYYGM DV	WGQGTTVTVSS	VH3
VH26	.....LY.Q...L.....			
D5	RVSMSVDMSRSQFFLELRDVTAADTAVYYCAR	DKGSEYSYFDP	WGQGIVVNVFS	VH4
IGHCAK	..TI...T.KN..S.K.SS.....			
A7	RVTITADDSTNTAYMGLSSLRSGDTAVYYCAR	VAYDGSGYYNNI PKIYYYSYMDV	WGKGTTVTVSS	VH1
VH1-69	.....K..S....E.....E.....			

FIG. 3C

Clone	Closest Germline	% amino acid homology	% nucleotide homology	R/S ratio FRs	R/S ratio CDRs
A4	DP-46	86	89	6/6:1.0	12/5:2.4
D2	DP-46	87	92	8/6:1.3	4/5:0.8
D121	DP-46	91	95	2/4:0.5	7/0:>7.0
B2	DP-7	67	79	20/17:1.2	14/5:2.8
D14	VH26	87	93	7/3:2.3	5/2:2.5
D5	IGHCAK	73	81	17/16:1.1	13/4:3.3
A7	VH1-69	90	94	7/2:3.5	5/0:>5.0

FIG. 4A

CDR's Heavy Chain

SEQ ID NO:	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3
15	SHGSH	22	LLSSDGSNKFYIESVKG	29	SLVGTTAFNY
16	..TM.	23	.IFY.....Y.AD....	30	.E..A...D.
17	.YTF.	24	VI.Y..NK.Y.AD....	31	.I........
18	GHHIH	25	RINPTGGGVSLAQSFQD	32	PRFNMIREPLDL
19	SYAMN	26	RISGNSGSTFYADSVKG	33	DLSSGAYYYYGMDV
20	GDSYFWS	27	RIYGRGTTNYNRVFGS	34	DKGSEYSYFDP
21	RYAIS	28	GIIPPFGPVNYAQKFQG	35	VAYDGSGYYNNIPKIYYYSYMDV

CDR's Light Chain

SEQ ID NO:	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3
36	KSSQSVFYTSNNKNYLA	43	WASTRES	50	QQYYDSYT
37	RASQGISSYLA	44	AASTLQS	51	QQLNSYPLT
38	RASQSVSSSYLA	45	GASSRAT	52	QQYGSSPRT
39	KSSQSVFYTSNNKNYLA	46	WASTRES	53	QQYYDSYT
40	RASQSVSSSYLA	47	GASSRAT	54	QQYDNVPDT
41	RASQSVSSSYLA	48	GASSRAT	55	QQYGTSPL
42	RASQSVSSSYLA	49	GASSRAT	56	QQYGSSPRT

FIG. 4B

Framework Regions, Heavy Chain

SEQ ID NO:	FR1	SEQ ID NO:	FR2
57	GGGVVQPGRSLKLSCAASGFTFS	64	WVRQAPGKGLEWVA
58	......AW..LR...V.......	64	.....
59	..........R..........	64	.....
60	GAEVRKPGTSVRISCRASGNTFT	65	WVRQAPGQGLQWMG
61	GGGLVQPGGSLRLSCATSGFIFN	66	WVRQAPGKGLEWVS
62	GPGLVRPSQTLSLTCPVSPGSIK	67	WVRQPVGKGLEWIG
63	GAEVKKPGSSVKVSCRASGGTFS	68	WVRQAPGQGLEWMG

SEQ ID NO:	FR3	SEQ ID NO:	FR4
69	RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI	76	WGQGTLVTVSS
70	.....R..........LS...PE.......TN	76	.....
71	.....VE.....	76	.....
72	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR	77	WGQGTVVTVSS
73	RFTISRDNSKNTAFLRMNSQRAEDTAVYYCAK	78	WGQGTTVTVSS
74	RVSMSVDMSRSQFFLELRDVTAADTAVYYCAR	79	WGQGIVVNVFS
75	RVTITADDSTNTAYMGLSSLRSGDTAVYYCAR	80	WGKGTTVTVSS

FIG. 4B cont'd

Framework Regions, Light Chain

SEQ ID NO:	FR1	SEQ ID NO:	FR2
81	PDSLAVSLGERATINC	88	WYQQKPGQPPKLLIY
82	PSFLSASVGDRVTITC	89	WYQLKPGKAPKLLIY
83	PGTLSLSPGERATLSC	90	WYQQKPGQAPRLLIY
84	PDSLAVSLGERATINC	91	WYQQKPGQPPKLLIY
85	PGTLSLSPGEGATLSC	92	WYQQRPGQAPRLLIY
86	PGTLSLSPGEGATLSC	93	WYQQKPGQAPRLLIY
87	PGTLSLSPGERVTLSC	94	WYQQKPGQAPRLLIY

SEQ ID NO:	FR3	SEQ ID NO:	FR4
95	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	102	FGQGTKLEIKRTVA
96	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	103	FGGGAKVGIRRTVA
97	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	104	FGQGTKVEIKRTVA
98	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	105	FGQGTKLEIKRTVA
99	GIPDRFSGSGSGTDFSFTISSLQPEDTGTYYC	106	FGQGTRLEIKRTVA
100	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	107	FGQGTRLEIKRTVA
101	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	108	FGQGTKVEIKRTVA

FIG. 5A

LIGHT CHAIN NUCLEOTIDE SEQUENCE OF ANTI-GPI ANTIBODIES

A4 – SEQ ID NO:112

CCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTTTACACTTCCAACAATAA
GAACTACTTAGCTTGGTACCAGCAGAAACCAGGCCAGCCTCCTAAGTTGCTCATTTACTGGGCATCCACCCGGGAATCCGGGGTCC
CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTAC
TGTCAGCAATATTATGATTCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCT

D2 – SEQ ID NO:113

CCATCCTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAAGGCATTAGCAGTTATTTAGCCTGGTAT
CAGCTAAAACCGGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAG
TGGATCTGGGACAGAATTCACTCTCACAATAAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTT
ACCCTCTCACTTTCGGCGGAGGGGCCAAGGTGGGGATCAGACGAACTGTGGCT

D121 – SEQ ID NO:114

CCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTG
GTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTG
GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGT
AG CTCACCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCT

B2 – SEQ ID NO:115

CCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTTTACACTTCCAACAATAA
GAACTACTTAGCTTGGTACCAGCAGAAACCAGGCCAGCCTCCTAAGTTGCTCATTTACTGGGCATCCACCCGGGAATCCGGGGTCC
CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTAC
TGTCAGCAATATTATGATTCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGAACTGTGGCT

FIG. 5A cont'd

D14 – SEQ ID NO:116

CCAGGCACCCTGTCATTGTCTCCAGGGGAAGGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACCTAGCCTG
GTATCAGCAGAGACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACCGGCATCCCAGACAGATTCAGTG
GAAGTGGATCTGGGACAGATTTCAGTTTCACCATCAGCAGTCTGCAGCCTGAAGATACTGGGACATATTACTGTCAACAATATGAT
AATGTCCCTGACACTTTTGGCCAGGGGACCAGGCTGGAGATCAAACGAACTGTGGCT

D5 – SEQ ID NO:117

CCAGGCACCCTGTCTTTGTCTCCAGGGGAAGGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTG
GTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGTAGGGCCACTGGCATCCCAGACAGGTTCAGTG
GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGT
ACCT CACCCCTCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTGGCT

A7 – SEQ ID NO:118

CCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGTCACTCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGTTACTTAGCCTG
GTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTG
GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGACTTTGCAGTTTATTACTGTCAGCAGTATGGA
AGCTCACCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCT

FIG. 5B

HEAVY CHAIN NUCLEOTIDE SEQUENCE OF ANTI-GPI ANTIBODIES

A4-H – SEQ ID NO:116

GAGGCGTGGTCCAGCCTGGGAGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACATTCAGTAGTCATGGCTCGCACTGGGTC
CGCCAAGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTTTGTCGTCTGATGGAAGTAATAAATTCTATATAGAATCCGTGAAGG
GCCGATTCACCATCTCCAAGGACAATTCTAAGAACACACTGTATCTGCAAATGAACAGCCTGAGAATTGACGACACGGCTGTCTAT
TACTGTGCGATTTCCCTGGTGGGAACTACCGCTTTTAACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

D2-H – SEQ ID NO:117

GGCGTGGTCCAAGCATGGAGGTCCCTAAGACTCTCCTGTGTAGCCTGTGGATTCACCTTCAGTAGTCATACCATGCACTGGGTCCG
CCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATATTCTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC
CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATTGAGCAGCCTAAGACCTGAGGACACGGCTGTCTATTA
TTGTACGAATTCCGAGGTGGGAGCTACCGCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG

D121-H – SEQ ID NO:118

GGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTTTTCCTGTGCAGCCTCTGGATTCACCTTCAGTTCCTATACTTTCCACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAACAAGAAATACTACGCAGACTCCGTGA
AGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACTCTATATCTGCAAATGAACAGCCTGAGAGTTGAGGACACGGCTGTT
TATTACTGTGCGATTTCCATAGTGGGAACTACCGCTTTTAACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC

B2-H – SEQ ID NO:119

GGGGCTGAGGGTGAGGAAGCCCGGACCTCCGTGAGGATCTCTTGCAGGGCATCTGGAAACACCTTCACTGGCCACCATATTCACTG
GGTCCGCCAGGCCCCTGGACAAGGCCTTCAGTGGATGGGAAGAATCAACCCGACTGGCGGCGGCGTTAGTCTCGCACAGAGTTTC
CAGGACAGAGTCAGCCTGACCAGGGACAGGTCGTCCAATACAGTCTTCTTGGAACTGAGCGGCCTCACGGAGGAGGACACGGCCT
TATATTTCTGTGCGAGGCCCCGATTTAACATGATCCGGGAACCTCTTGACCTCTGGGGCCAGGGGACAGTGGTCACCGTCTCCTCA

D14-H – SEQ ID NO:120

GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAACCTCTGGATTCATCTTTAACAGCTATGCCATGAACTG
GGTCCGCCAGGCTCCAGGGAAGGGGCTTGAGTGGGTCTCACGTATTAGTGGAAATAGTGGAAGCACATTCTACGCAGACTCCGTG
AAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGGCGTTTCTGCGAATGAACAGCCAGAGAGCCGAAGACACGGCCG
TTTATTACTGTGCGAAAGATCTGTCGAGTGGTGCATACTACTACTACGGGATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTC
TCCTCA

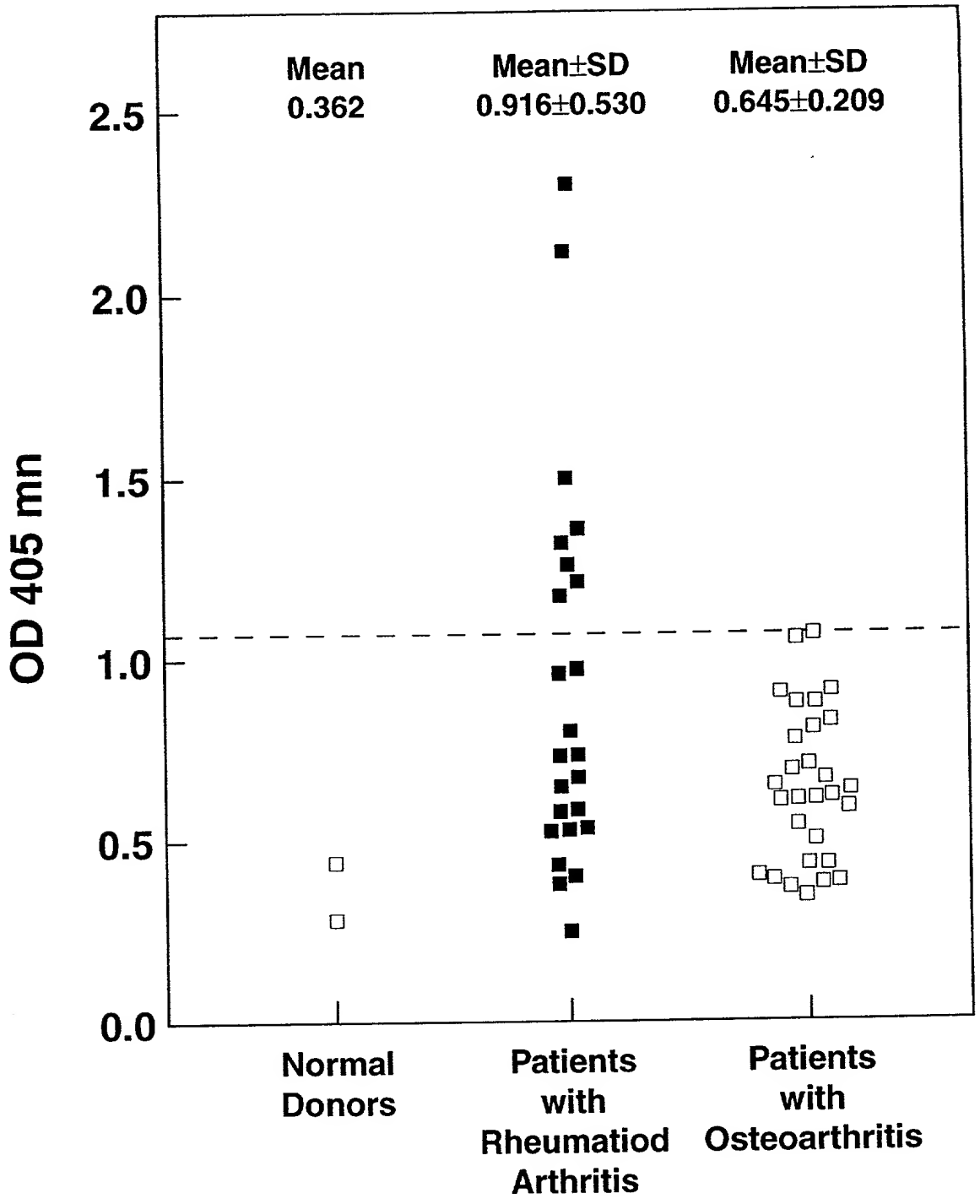
D5-H – SEQ ID NO:121

GGCCCAGGATTGGTGAGGCCATCACAGACCCTATCCCTCACCTGCACTGTCTCTCCAGGCTCCATTAAAGGTGATAGTTACTTCTGG
AGCTGGGTCCGTCAGCCCGTAGGGAAGGGACTGGAGTGGATAGGGCGTATCTACGGCAGAGGGACTACCAATTACAACCGTGTTT
TCGGGAGTCGAGTCAGTATGTCAGTGGACATGTCCAGGAGTCAGTTTTTCTTGGAATTGAGAGATGTGACCGCCGCAGACACGGCC
GTCTATTACTGTGCGAGAGACAAGGGGTCCGAATACTCCTACTTTGACCCCTGGGGCCAGGGAATAGTGGTCAACGTCTTCTCA

FIG. 5B CONT'D

A7-H – SEQ ID NO:122

GGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAGGGCTTCTGGAGGCACATTCAGCAGATATGCTA
TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTCCCTTTGGTCCAGTAAACT
ACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGATTCCACGAACACAGCCTACATGGGTCTGAGCAGCC
TGAGATCTGGGGACACGGCCGTGTATTACTGCGCGAGAGTGGCCTATGATGGTAGTGGCTATTACAACAATATCCCAA
AGATCTACTACTACTCCTACATGGACGTCTGGGGCAAAGGGACCACGGTCACCGTGTCCTCAGC


Mean
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Mean±SD
0.916±0.530
Mean±SD
0.645±0.209
2.5
2.0
1.5
1.0
0.5
0.0
OD 405 mn
Normal Donors
Patients with Rheumatiod Arthritis
Patients with Osteoarthritis

Fig. 6

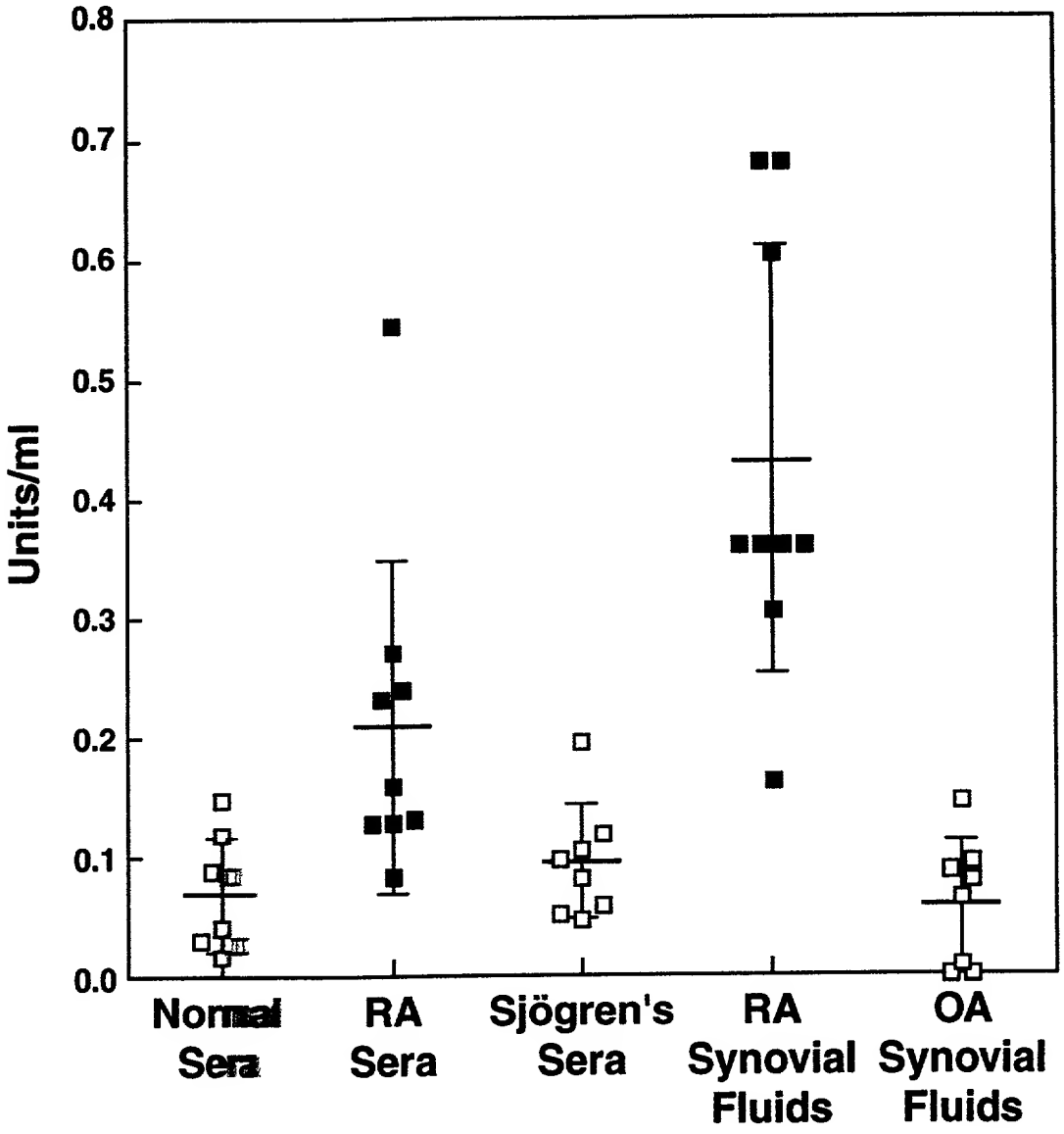
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Units/ml
Normal Sera
RA Sera
Sjögren's Sera
RA Synovial Fluids
OA Synovial Fluids

Fig. 7

TOSOH" 8023860

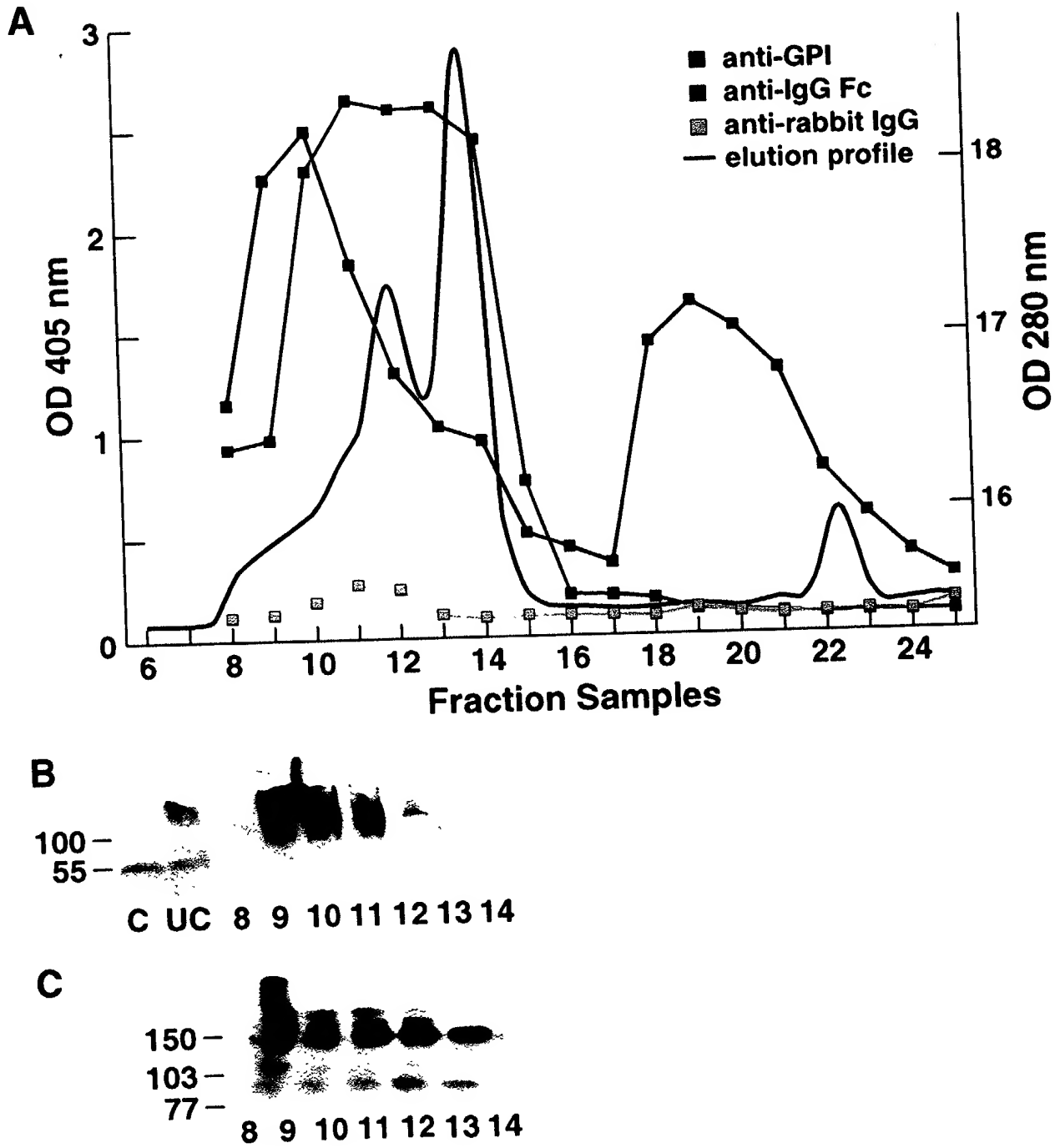

Fig. 8

TRANSLATED DOCUMENT
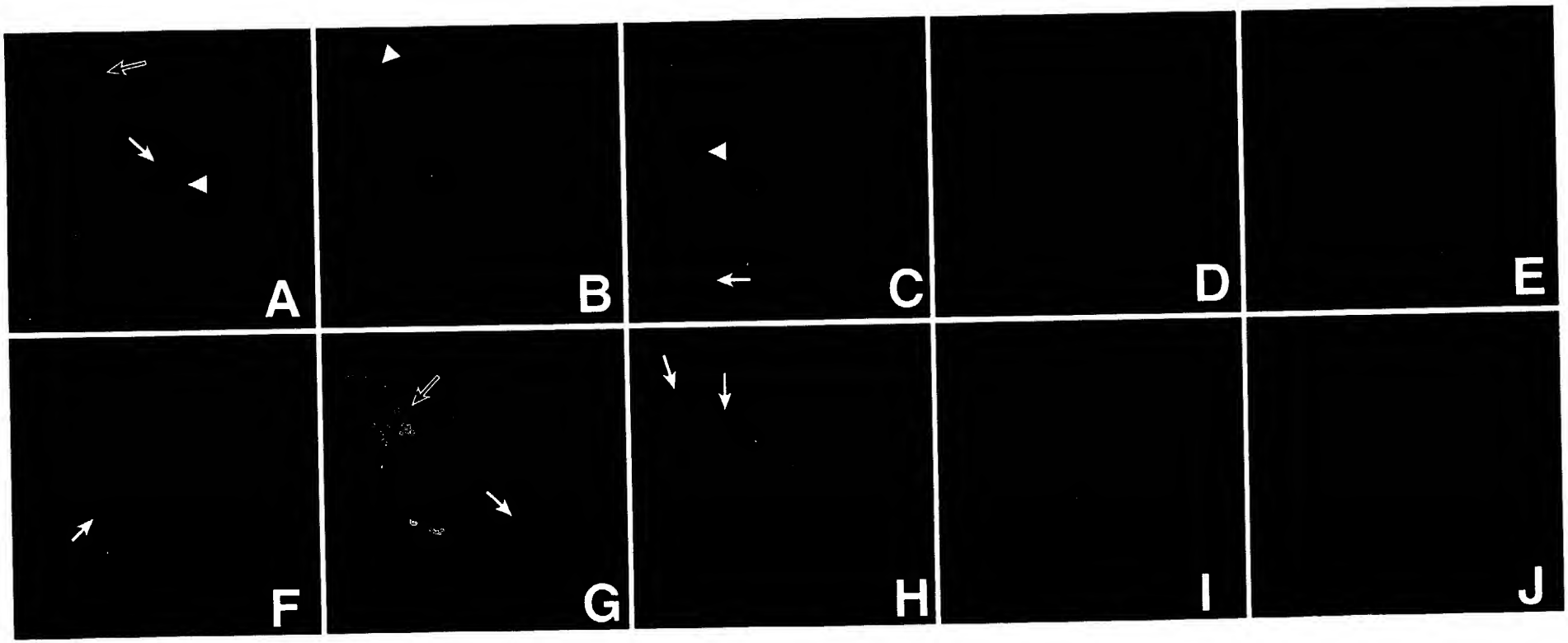
Fig 9